

GenCore version 5.1.4-p5-4578
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OM protein - protein search, using sw model

Run on: March 20, 2003, 08:20:06 ; Search time 0.001 Seconds

(without alignments)
858.346 Million cell updates/sec

Title: us-09-488-265-26
2470

Perfect score: 1 MGVEVLLSIATLFGSTSGT.....DFVEGLSFARSGNMECEFA 467

Sequence: 1 MGVEVLLSIATLFGSTSGT.....DFVEGLSFARSGNMECEFA 467

Scoring table: BIOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 4 seqs, 1838 residues

Total number of hits satisfying chosen parameters: 4

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : ramirez126.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2470	100.0	467	1	US-09-343-126C-129
2	2448	99.1	467	1	US-09-343-126C-134
3	2342	94.8	467	1	US-09-343-126C-132
4	2115	85.6	437	1	US-09-343-126C-130

ALIGNMENTS

RESULT 1

US-09-343-126C-129

; Sequence 129, Application US/09343126C
; GENERAL INFORMATION:
; APPLICANT: Brugger, Roland
; APPLICANT: Lehmann, Martin
; APPLICANT: Wyss, Markus
; TITLE OF INVENTION: Phytase Formulations
; FILE REFERENCE: C38435/109741
; CURRENT APPLICATION NUMBER: US/09/343,126C
; CURRENT FILING DATE: 1999-06-29
; NUMBER OF SEQ ID NOS: 139
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 129
; LENGTH: 467
; TYPE: PRT
; ORGANISM: Consensus sequence
US-09-343-126C-129

Query Match 100.0%; Score 2470; DB 1; Length 467;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 467; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MGVEVLLSIATLFGSTSGTALGPRGNHSCDVTGQYGCPEISHLMGQYSPFSLADE 60

Db 1 MGVEVLLSIATLFGSTSGTALGPRGNHSCDVTGQYGCPEISHLMGQYSPFSLADE 60
QY 61 SAISPDVPRKGRVTFVQVLSRHGARYPTSSKSKRYSALEIAIQRNATAFRGKVAFLKTYN 120
Db 61 SAISPDVPRKGRVTFVQVLSRHGARYPTSSKSKRYSALEIAIQRNATAFRGKVAFLKTYN 120
QY 121 YTLGADDLTPFGEOQMVNSGKIFRRYKALARKIVPEVRASGSDRVYASAEKEIEGQSA 180
Db 121 YTLGADDLTPFGEOQMVNSGKIFRRYKALARKIVPEVRASGSDRVYASAEKEIEGQSA 180
QY 181 KLADPGANPHQASPVINVIIEGAGYNNITLDHGLCTAFEESELGDDVEANFTAVFAPPIR 240
Db 181 KLADPGANPHQASPVINVIIEGAGYNNITLDHGLCTAFEESELGDDVEANFTAVFAPPIR 240
QY 241 ARLEAHLPGVNLTDEEDVNNLMDKCPFTVARTSDATQLSFCDLFTHDEWIOYDYLSIG 300
Db 241 ARLEAHLPGVNLTDEEDVNNLMDKCPFTVARTSDATQLSFCDLFTHDEWIOYDYLSIG 300
QY 301 KYGYGAGNPLGPAQGVFNELIARLTHSPVODHTSTNTTLDNPAATPLNATLYADS 360
Db 301 KYGYGAGNPLGPAQGVFNELIARLTHSPVODHTSTNTTLDNPAATPLNATLYADS 360
QY 361 HDNTMWSIFFALGLYNGTKPLSTTSVESIEETDGYAASWTVPARAYVEMQCEAEKEP 420
Db 361 HDNTMWSIFFALGLYNGTKPLSTTSVESIEETDGYAASWTVPARAYVEMQCEAEKEP 420
QY 421 LVRLVNDRVVPLHGGGVNKLGRCKRDPFEGISFARSGNMECEFA 467
Db 421 LVRLVNDRVVPLHGGGVNKLGRCKRDPFEGISFARSGNMECEFA 467

RESULT 2

US-09-343-126C-134

; Sequence 134, Application US/09343126C
; GENERAL INFORMATION:
; APPLICANT: Brugger, Roland
; APPLICANT: Lehmann, Martin
; APPLICANT: Wyss, Markus
; TITLE OF INVENTION: Phytase Formulations
; FILE REFERENCE: C38435/109741
; CURRENT APPLICATION NUMBER: US/09/343,126C
; CURRENT FILING DATE: 1999-06-29
; NUMBER OF SEQ ID NOS: 139
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 134
; LENGTH: 467
; TYPE: PRT
; ORGANISM: Consensus sequence
US-09-343-126C-134

Query Match 99.1%; Score 2448; DB 1; Length 467;
Best Local Similarity 98.9%; Pred. No. 0;
Matches 462; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
QY 1 MGVEVLLSIATLFGSTSGTALGPRGNHSCDVTGQYGCPEISHLMGQYSPFSLADE 60
Db 1 MGVEVLLSIATLFGSTSGTALGPRGNHSCDVTGQYGCPEISHLMGQYSPFSLADE 60
QY 61 SAISPDVPRKGRVTFVQVLSRHGARYPTSSKSKRYSALEIAIQRNATAFRGKVAFLKTYN 120
Db 61 SAISPDVPRKGRVTFVQVLSRHGARYPTSSKSKRYSALEIAIQRNATAFRGKVAFLKTYN 120
QY 121 YTLGADDLTPFGEOQMVNSGKIFRRYKALARKIVPEVRASGSDRVYASAEKEIEGQSA 180
Db 121 YTLGADDLTPFGEOQMVNSGKIFRRYKALARKIVPEVRASGSDRVYASAEKEIEGQSA 180
QY 181 KLADPGANPHQASPVINVIIEGAGYNNITLDHGLCTAFEESELGDDVEANFTAVFAPPIR 240
Db 181 KLADPGANPHQASPVINVIIEGAGYNNITLDHGLCTAFEESELGDDVEANFTAVFAPPIR 240
QY 241 ARLEAHLPGVNLTDEEDVNNLMDKCPFTVARTSDATQLSFCDLFTHDEWIOYDYLSIG 300
Db 241 ARLEAHLPGVNLTDEEDVNNLMDKCPFTVARTSDATQLSFCDLFTHDEWIOYDYLSIG 300

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Db      241 ARLEAHLPGVNLDEEDVYVNLMDMCEPDVARTSDATQLSPECDLFTHDEWIQYDYLSIG 300
QY      301 KYIYGAGNPLPGAGVGVVNNELIARLTHSPQODHTSTNHTLDSNPATFPLNATLYADFS 360
Db      301 KYIYGAGNPLPGAGVGVVNNELIARLTHSPQODHTSTNHTLDSNPATFPLNATLYADFS 360
QY      361 HNDTWISIFPALGLYNGTGPLSTTSVESIEETDGYAASWTVFPAARAYEMMOCEAKEP 420
Db      361 HNDTWISIFPALGLYNGTGPLSTTSVESIEETDGYAASWTVFPAARAYEMMOCEAKEP 420
QY      421 LVRLVNDRVVPLHGGCVGVDKLGCRKRDVEGLSFARSGNMEECEFA 467
Db      421 LVRLVNDRVVPLHGGCVGVDKLGCRKRDVEGLSFARSGNMEECEFA 467

RESULT 3
US-09-343-126C-132
; Sequence 132, Application US/09343126C
; GENERAL INFORMATION:
; APPLICANT: Brugger, Roland
; APPLICANT: Lehmann, Martin
; APPLICANT: Wyss, Markus
; TITLE OF INVENTION: Phytase Formulations
; FILE REFERENCE: C38435/109741
; CURRENT APPLICATION NUMBER: US/09/343,126C
; CURRENT FILING DATE: 1999-06-29
; NUMBER OF SEQ ID NOS: 139
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 132
; LENGTH: 467
; TYPE: PRT
; ORGANISM: Consensus sequence
US-09-343-126C-132

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Query Match      94.8%; Score 2342; DB 1; Length 467;
Best Local Similarity 94.4%; Pred. No. 0;
Matches 441; Conservative 10; Mismatches 16; Indels 0; Gaps 0;

QY      1 MGVEVVLISITLFGSTSGTALGPRGNSHSCDVTVDGGYQCFPEISHLMGQYSPFSLADE 60
Db      1 MGVEVVLISITLFGSTSGTALGPRGNSHSCDVTVDGGYQCFPEISHLMGQYSPFSLADE 60
QY      61 SAISPDVPGKGRVTFVOYLSRHGARYPTSSSKRYTSALIRAIQKNATAFKGYAFLKTYN 120
Db      61 SAISPDVPGKGRVTFVOYLSRHGARYPTSSSKRYTSALIRAIQKNATAFKGYAFLKTYN 120
QY      121 YTLGADDLTPREGOMVNSGIKFFRRYKALARKIVPEVRASGSDRVIASAEKTEGFOSA 180
Db      121 YTLGADDLTPREGOMVNSGIKFFRRYKALARKIVPEVRASGSDRVIASAEKTEGFOSA 180
QY      121 YTLGADDLTPREGOMVNSGIKFFRRYKALARKIVPEVRASGSDRVIASAEKTEGFOSA 180
Db      121 YTLGADDLTPREGOMVNSGIKFFRRYKALARKIVPEVRASGSDRVIASAEKTEGFOSA 180
QY      181 KLADPGANPHQASPIVNIYIPEGAGYNTLIDHGLCTAFEESELGDDVYANFTAVFAPPIR 240
Db      181 KLADPGANPHQASPIVNIYIPEGAGYNTLIDHGLCTAFEESELGDDVYANFTAVFAPPIR 240
QY      241 ARLEAHLPGVNLDEEDVYVNLMDMCEPDVARTSDATQLSPECDLFTHDEWIQYDYLSIG 300
Db      241 ARLEAHLPGVNLDEEDVYVNLMDMCEPDVARTSDATQLSPECDLFTHDEWIQYDYLSIG 300
QY      301 KYIYGAGNPLPGAGVGVVNNELIARLTHSPQODHTSTNHTLDSNPATFPLNATLYADFS 360
Db      301 KYIYGAGNPLPGAGVGVVNNELIARLTHSPQODHTSTNHTLDSNPATFPLNATLYADFS 360
QY      361 HNDTWISIFPALGLYNGTGPLSTTSVESIEETDGYAASWTVFPAARAYEMMOCEAKEP 420
Db      361 HNDTWISIFPALGLYNGTGPLSTTSVESIEETDGYAASWTVFPAARAYEMMOCEAKEP 420
QY      421 LVRLVNDRVVPLHGGCVGVDKLGCRKRDVEGLSFARSGNMEECEFA 467
Db      421 LVRLVNDRVVPLHGGCVGVDKLGCRKRDVEGLSFARSGNMEECEFA 467

```

RESULT 4
US-09-343-126C-130

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; Sequence 130, Application US/09343126C
; GENERAL INFORMATION:
; APPLICANT: Brugger, Roland
; APPLICANT: Lehmann, Martin
; APPLICANT: Wyss, Markus
; TITLE OF INVENTION: Phytase Formulations
; FILE REFERENCE: C38435/109741
; CURRENT APPLICATION NUMBER: US/09/343,126C
; CURRENT FILING DATE: 1999-06-29
; NUMBER OF SEQ ID NOS: 139
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 130
; LENGTH: 437
; TYPE: PRT
; ORGANISM: Consensus sequence
US-09-343-126C-130

Query Match      85.6%; Score 2115; DB 1; Length 437;
Best Local Similarity 93.5%; Pred. No. 0;
Matches 419; Conservative 2; Mismatches 9; Indels 18; Gaps 10;

QY      27 NSHSCDVTVDGGYQCFPEISHLMGQYSPFSLADESAISPDVPGKGRVTFVOYLSRHGARY 86
Db      1 NSHSCDVTVD-GYQC-PEISHLMGQYSPFSLADESAISPDVPGKGRVTFVOYLSRHGARY 58
QY      87 PTSSSKRYTSALIRAIQKNATAFKGYAFLKTYNVTLGADDLTPREGOMVNSGIKFFRR 146
Db      59 PTSSSKRYTSALIRAIQKNAT-FKGYAFLKTYNVTLGADDLTPREGOMVNSGIKFFRR 117
QY      147 YKALARKIVPEVRASGSDRVIASAEKTEGFOSA KLADPGANPHQASPIVNIYIPEGAGY 206
Db      118 YKALARKIVPEVRASGSDRVIASAEKTEGFOSA KLADPA--HQASPIVNIYIPEGAGY 174
QY      207 NNTLDHGLCTAFEESELGDDVYANFTAVFAPPIRARIARLEAHLPGVNLDEEDVYVNLMDMCEP 266
Db      175 NNTLDHGLCTAFEESELGDDVYANFTAVFAPPIRARIARLEAHLPGVNLDEEDVYVNLMDMCEP 233
QY      267 DTVARTSDATQLSPECDLFTHDEWIQYDYLSIGKRYGAGNPLPGAGVGVVNNELIAR 326
Db      234 DTVARTSDATQLSPECDLFTHDEWIQYDYLSIGL-KRYGAGNPLPGAGVGV--NELIAR 290
QY      327 LTHSPVQODHTSTNHTLDSNPATFPLNATLYADFSHNDTWISIFPALGLYNGTGPLSTTSV 386
Db      291 LTHSPVQODHTSTNHTLDSNPATFPLNATLYADFSHNDTWISIFPALGLYNGTGPLSTTSV 350
QY      387 ESIEETDGYAASWTVFPAARAYEMMOCEA-----EKEPLVRLVNDRVVPLHGGCVD 439
Db      351 ESIEETDGYAASWTVFPAARAYEMMOCEA-----EKEPLVRLVNDRVVPLHGGCVD 409
QY      440 KLGRCKRDVEGLSFARSGNMEECEFA 467
Db      410 KLGRCKRDVEGLSFARSGNMEECEFA 437

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Search completed: March 20, 2003, 08:20:07
Job time : 1 secs

GenCore version 5.1.4-p5-4578
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OM protein - protein search, using sw model

Run on: March 20, 2003, 08:22:01 ; Search time 0.001 Seconds
(without alignments)
803.206 Million cell updates/sec

Title: us-09-488-265-27

Perfect score: 2321

Sequence: 1 NSHSCDVTVDGYQCPEISHLMGOYSPFFSLADESAISPDPVKGCRTVTVQVLSRHGARYPT 437

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 4 seqs, 1838 residues

Total number of hits satisfying chosen parameters: 4

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : ramirez126.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2321	100.0%	437	1	US-09-343-126C-130
2	2115	91.1	467	1	US-09-343-126C-129
3	2093	90.2	467	1	US-09-343-126C-134
4	2044	88.1	467	1	US-09-343-126C-132

ALIGNMENTS

RESULT 1
US-09-343-126C-130
; Sequence 130, Application US/09343126C
; GENERAL INFORMATION:
; APPLICANT: Brugger, Roland
; APPLICANT: Lehmann, Martin
; APPLICANT: Wyss, Markus
; TITLE OF INVENTION: Phytase Formulations
; FILE REFERENCE: C38435/109741
; CURRENT APPLICATION NUMBER: US/09/343,126C
; CURRENT FILING DATE: 1999-06-23
; NUMBER OF SEQ ID NOS: 139
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 130
; LENGTH: 437
; TYPE: PRT
; ORGANISM: Consensus sequence
US-09-343-126C-130

Query Match 100.0%; Score 2321; DB 1; Length 437;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 437; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 NSHSCDVTVDGYQCPEISHLMGOYSPFFSLADESAISPDPVKGCRTVTVQVLSRHGARYPT 60

Db 1 NSHSCDVTVDGYQCPEISHLMGOYSPFFSLADESAISPDPVKGCRTVTVQVLSRHGARYPT 60
Oy 61 SSKSKKYSALLERICKNATFKKRYAFKTYNTTLCADLLTPGEGNOMVNSGKIFYRRYA 120
Db 61 SSKSKKYSALLERICKNATFKKRYAFKTYNTTLCADLLTPGEGNOMVNSGKIFYRRYA 120
Oy 121 LARNIVPEFVRASGSDRVIASAEKFTIEGQSAKLADPAHQASPVIVTIIPEGSGYNTLDDH 180
Db 121 LARNIVPEFVRASGSDRVIASAEKFTIEGQSAKLADPAHQASPVIVTIIPEGSGYNTLDDH 180
Oy 181 GLCTAFEDSTIGDDEANFTAVFAPPIRARLEALPGVNLTDDEVYVNLMDMCPDPTVARTS 240
Db 181 GLCTAFEDSTIGDDEANFTAVFAPPIRARLEALPGVNLTDDEVYVNLMDMCPDPTVARTS 240
Oy 241 DATOLSPFCDLFTADEMOYDYLOSILKYVGAGNPLGPAQGVGNELIARLTHSPVDHT 300
Db 241 DATOLSPFCDLFTADEMOYDYLOSILKYVGAGNPLGPAQGVGNELIARLTHSPVDHT 300
Oy 301 STNHTLDSNPATFPLNATLYADFSDHNTMVSIFPALGLYNGTKPLSTTSVESIETDGYAA 360
Db 301 STNHTLDSNPATFPLNATLYADFSDHNTMVSIFPALGLYNGTKPLSTTSVESIETDGYAA 360
Oy 361 SMTVPFAARAYVEMQCCAGGGGGBGKEPLRVRLVNDRVVPLHGGVDKLGKCKLDDFV 420
Db 361 SMTVPFAARAYVEMQCCAGGGGGBGKEPLRVRLVNDRVVPLHGGVDKLGKCKLDDFV 420
Oy 421 EGLSFARSGGNMAECFA 437
Db 421 EGLSFARSGGNMAECFA 437

RESULT 2
US-09-343-126C-129
; Sequence 129, Application US/09343126C
; GENERAL INFORMATION:
; APPLICANT: Brugger, Roland
; APPLICANT: Lehmann, Martin
; APPLICANT: Wyss, Markus
; TITLE OF INVENTION: Phytase Formulations
; FILE REFERENCE: C38435/109741
; CURRENT APPLICATION NUMBER: US/09/343,126C
; CURRENT FILING DATE: 1999-06-23
; NUMBER OF SEQ ID NOS: 139
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 129
; LENGTH: 467
; TYPE: PRT
; ORGANISM: Consensus sequence
US-09-343-126C-129

Query Match 91.1%; Score 2115; DB 1; Length 467;
Best Local Similarity 93.5%; Pred. No. 0;
Matches 419; Conservative 2; Mismatches 9; Indels 10; Gaps 10;

Oy 1 NSHSCDVTVD-GYQC-PEISHLMGOYSPFFSLADESAISPDPVKGCRTVTVQVLSRHGARY 58
Db 27 NSHSCDVTVDGYQCPEISHLMGOYSPFFSLADESAISPDPVKGCRTVTVQVLSRHGARY 86
Oy 59 PTSSKSKYSALLERICKNAT-FKGRYAFKTYNTTLCADLLTPGEGNOMVNSGKIFYRR 117
Db 87 PTSSKSKYSALLERICKNATFKKRYAFKTYNTTLCADLLTPGEGNOMVNSGKIFYRR 146
Oy 118 YKALARNIVPEFVRASGSDRVIASAEKFTIEGQSAKLADPA--HQASPVIVNIIPEGSGY 174
Db 147 YKALARNIVPEFVRASGSDRVIASAEKFTIEGQSAKLADPAHQASPVIVNIIPEGSGY 206
Oy 175 NNTLDDGICTAPEFDSLTGDAEANTFVAPPIRARLEA-LRGVNLTDDEVYVNLMDMCP 233
Db 207 NNTLDDGICTAPEFDSLTGDAEANTFVAPPIRARLEA-LRGVNLTDDEVYVNLMDMCP 266
Oy 234 DTVAATSDATOLSPFCDLFTADEM-OYDYLOSIL-KYVGAGNPLGPAQGVGNELIAR 290

Db 267 DTVARTSDATQUSPFCDLFTHDEWIQYDYLQSLGKYYGAGNPLGPAQGVGFVNNELIAR 326
QY 291 LTHSPVODHTSTNHTLDSNPATFPLNATLYADFSHDNTMWSIFFALGLYNGTKPLSTTSV 350
Db 327 LTHSPVODHTSTNHTLDSNPATFPLNATLYADFSHDNTMWSIFFALGLYNGTKPLSTTSV 386
QY 351 EST-ETDGYAASWTVPFAARAIVEMMOCEAGGGEKEPELVRLVNDRVVPLHGGVD 409
Db 387 ESTEETDGYAASWTVPFAARAIVEMMOCEA-----EKEPLVRLVNDRVVPLHGGVD 439
QY 410 KLGRCKLDPEVEGLSFARSGNMMAECFA 437
Db 440 KLGRCKRDPFVEGLSFARSGNMMECFA 467

RESULT 3
US-09-343-126C-134
; Sequence 134, Application US/09343126C
; GENERAL INFORMATION:
; APPLICANT: Brugger, Roland
; APPLICANT: Lehmann, Martin
; APPLICANT: Wyss, Markus
; TITLE OF INVENTION: Phytase Formulations
; FILE REFERENCE: C38435/109741
; CURRENT APPLICATION NUMBER: US/09/343,126C
; CURRENT FILING DATE: 1999-06-29
; NUMBER OF SEQ ID NOS: 139
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 134
; LENGTH: 467
; TYPE: PRT
; ORGANISM: Consensus sequence
US-09-343-126C-134

Query Match 90.2%; Score 2093; DB 1; Length 467;
Best Local Similarity 92.4%; Pred. No. 0;
Matches 414; Conservative 4; Mismatches 12; Indels 18; Gaps 10;

QY 1 NSHSCDTVD-GYOC-PEISHLMGOYSPFSLADESAISPDVPGKCVTFVQVLSRHGARY 58
Db 27 NSHSCDTVDGGOCPFPEISHLMGOYSPFSLADESAISPDVPGKCVTFVQVLSRHGARY 86
QY 59 PTSSKSKYSALIERIOKNAT-FKGYAFLKTYNTYLGADDLPPFGENOMVNSGKIFRYR 117
Db 87 PTSSASAKYSALIERIOKNATFAKGYAFLKTYNTYLGADDLPPFGENOMVNSGKIFRYR 146
QY 118 YKALARNIVPFVRASGSDRYIASAEKFEIGFOSAKLADPA---HQASPVINVIIPESGY 174
Db 147 YKALARKIVPFIRASGSDRYIASAEKFEIGFOSAKLADPGANPHQASPVINVIIPESGAGY 206
QY 175 NNTLDHGLCTAFEDSTIGDGAENFTAVFAPPIRARLEA-LPGVNLDEDEVNLMDCPF 233
Db 207 NNTLDHGLCTAFEDSELDGDEANFTAVFAPPIRARLEALPGVNLDEDEVNLMDCPF 266
QY 234 DTVARTSDATQUSPFCDLFTADEW-QYDYLOSL-KYYGYGAGNPLGPAQGVGF-NELIAR 290
Db 267 DTVARTSDATQUSPFCDLFTADEWQYDYLOSL-KYYGYGAGNPLGPAQGVGFVNNELIAR 326
QY 291 LTHSPVODHTSTNHTLDSNPATFPLNATLYADFSHDNTMWSIFFALGLYNGTKPLSTTSV 350
Db 327 LTHSPVODHTSTNHTLDSNPATFPLNATLYADFSHDNTMWSIFFALGLYNGTKPLSTTSV 386
QY 351 EST-ETDGYAASWTVPFAARAIVEMMOCEAGGGEKEPELVRLVNDRVVPLHGGVD 409
Db 387 ESTEETDGYAASWTVPFAARAIVEMMOCEA-----EKEPLVRLVNDRVVPLHGGVD 439
QY 410 KLGRCKLDPEVEGLSFARSGNMMAECFA 437
Db 440 KLGRCKRDPFVEGLSFARSGNMMECFA 467

RESULT 4
US-09-343-126C-132

; Sequence 132, Application US/09343126C
; GENERAL INFORMATION:
; APPLICANT: Brugger, Roland
; APPLICANT: Lehmann, Martin
; APPLICANT: Wyss, Markus
; TITLE OF INVENTION: Phytase Formulations
; FILE REFERENCE: C38435/109741
; CURRENT APPLICATION NUMBER: US/09/343,126C
; CURRENT FILING DATE: 1999-06-29
; NUMBER OF SEQ ID NOS: 139
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 132
; LENGTH: 467
; TYPE: PRT
; ORGANISM: Consensus sequence
US-09-343-126C-132

Query Match 88.1%; Score 2044; DB 1; Length 467;
Best Local Similarity 90.4%; Pred. No. 0;
Matches 405; Conservative 7; Mismatches 18; Indels 18; Gaps 10;

QY 1 NSHSCDTVD-GYOC-PEISHLMGOYSPFSLADESAISPDVPGKCVTFVQVLSRHGARY 58
Db 27 NSHSCDTVDGGOCPFPEISHLMGOYSPFSLADESAISPDVPGKCVTFVQVLSRHGARY 86
QY 59 PTSSKSKYSALIERIOKNAT-FKGYAFLKTYNTYLGADDLPPFGENOMVNSGKIFRYR 117
Db 87 PTSSASAKYSALIERIOKNATFAKGYAFLKTYNTYLGADDLPPFGENOMVNSGKIFRYR 146
QY 118 YKALARNIVPFVRASGSDRYIASAEKFEIGFOSAKLADPA---HQASPVINVIIPESGY 174
Db 147 YKALARKIVPFIRASGSDRYIASAEKFEIGFOSAKLADPGANPHQASPVINVIIPESGY 206
QY 175 NNTLDHGLCTAFEDSTIGDGAENFTAVFAPPIRARLEA-LPGVNLDEDEVNLMDCPF 233
Db 207 NNTLDHGLCTAFEDSELDGDEANFTAVFAPPIRARLEALPGVNLDEDEVNLMDCPF 266
QY 234 DTVARTSDATQUSPFCDLFTADEW-QYDYLOSL-KYYGYGAGNPLGPAQGVGF-NELIAR 290
Db 267 DTVARTSDATQUSPFCDLFTADEWQYDYLOSL-KYYGYGAGNPLGPAQGVGFVNNELIAR 326
QY 291 LTHSPVODHTSTNHTLDSNPATFPLNATLYADFSHDNTMWSIFFALGLYNGTKPLSTTSV 350
Db 327 LTHSPVODHTSTNHTLDSNPATFPLNATLYADFSHDNTMWSIFFALGLYNGTKPLSTTSV 386
QY 351 EST-ETDGYAASWTVPFAARAIVEMMOCEAGGGEKEPELVRLVNDRVVPLHGGVD 409
Db 387 ESTEETDGYAASWTVPFAARAIVEMMOCEA-----EKEPLVRLVNDRVVPLHGGVD 439
QY 410 KLGRCKLDPEVEGLSFARSGNMMAECFA 437
Db 440 KLGRCKRDPFVEGLSFARSGNMMECFA 467

Search completed: March 20, 2003, 08:22:01
Job time : 0.001 secs

GenCore version 5.1.4.p5_4578
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OM protein - protein search, using sw model

Run on: March 20, 2003, 08:23:05 ; Search time 0.001 Seconds

(without alignments)
858.346 Million cell updates/sec

Title: us-09-488-265-29

Perfect score: 2462

Sequence: 1 MGFEVLLSLATLFGSTSGTALGP...DEVEGLSFARSGGNMAECFA 467

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 4 seqs, 1838 residues

Total number of hits satisfying chosen parameters: 4

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : ramirez126.pep.*

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2462	100.0	467	1	US-09-343-126C-132
2	2362	95.9	467	1	US-09-343-126C-134
3	2342	95.1	467	1	US-09-343-126C-129
4	2044	83.0	437	1	US-09-343-126C-130

ALIGNMENTS

RESULT 1
US-09-343-126C-132

; Sequence 132, Application US/09343126C

; GENERAL INFORMATION:

; APPLICANT: Brugger, Roland

; APPLICANT: Lehmann, Martin

; APPLICANT: Wysz, Markus

; TITLE OF INVENTION: Phytase Formulations

; FILE REFERENCE: C38435/109741

; CURRENT APPLICATION NUMBER: US/09/343.126C

; CURRENT FILING DATE: 1999-06-29

; NUMBER OF SEQ ID NOS: 139

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 132

; LENGTH: 467

; TYPE: PRT

; ORGANISM: Consensus sequence

US-09-343-126C-132

Query Match 100.0%; Score 2462; DB 1; Length 467;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 467; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGFEVLLSLATLFGSTSGTALGP...DEVEGLSFARSGGNMAECFA 60

```

Db      1 MGFEVLLSLATLFGSTSGTALGP...DEVEGLSFARSGGNMAECFA 60
QY      61 SAISPDVDDCRVTFVQVLSRHGARYPTSSAKVSALEALQKNAFAKGYAFKTYN 120
Db      61 SAISPDVDDCRVTFVQVLSRHGARYPTSSAKVSALEALQKNAFAKGYAFKTYN 120
QY      121 YTLGADDLTPFGGNQVNSGIFKFRYKALARKIYVFIASGSDRYASAEKFIQFQSA 180
Db      121 YTLGADDLTPFGGNQVNSGIFKFRYKALARKIYVFIASGSDRYASAEKFIQFQSA 180
QY      181 KLADPGSPHQASPVYINVIIPGSGYNNLTLDGCTAFEDSELGDVQVNAFALFAPAIR 240
Db      181 KLADPGSPHQASPVYINVIIPGSGYNNLTLDGCTAFEDSELGDVQVNAFALFAPAIR 240
QY      241 ARLEADLPQVTLTDEDDVYIYLMDCPFDVARTSDATELSPFCALFTHDEWIQDYLSIG 300
Db      241 ARLEADLPQVTLTDEDDVYIYLMDCPFDVARTSDATELSPFCALFTHDEWIQDYLSIG 300
QY      301 KYGGAGNPLGPAQGVFANELIARLTHSPVQDHTNNHLLDSNPATFPLNATLYADFS 360
Db      301 KYGGAGNPLGPAQGVFANELIARLTHSPVQDHTNNHLLDSNPATFPLNATLYADFS 360
QY      361 HNTMISIFPALGLYNGTKPLSTTSVESIEETDGYASAWTPFARAVEMQCAKEP 420
Db      361 HNTMISIFPALGLYNGTKPLSTTSVESIEETDGYASAWTPFARAVEMQCAKEP 420
QY      421 LVRLVNDRVVPLHGCNADKLGRCRDFVAGLSFARSGGNMAECFA 467
Db      421 LVRLVNDRVVPLHGCNADKLGRCRDFVAGLSFARSGGNMAECFA 467

```

RESULT 2

US-09-343-126C-134

; Sequence 134, Application US/09343126C

; GENERAL INFORMATION:

; APPLICANT: Brugger, Roland

; APPLICANT: Lehmann, Martin

; APPLICANT: Wysz, Markus

; TITLE OF INVENTION: Phytase Formulations

; FILE REFERENCE: C38435/109741

; CURRENT APPLICATION NUMBER: US/09/343.126C

; CURRENT FILING DATE: 1999-06-29

; NUMBER OF SEQ ID NOS: 139

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 134

; LENGTH: 467

; TYPE: PRT

; ORGANISM: Consensus sequence

US-09-343-126C-134

Query Match 95.9%; Score 2362; DB 1; Length 467;

Best Local Similarity 95.5%; Pred. No. 0;

Matches 446; Conservative 8; Mismatches 13; Indels 0; Gaps 0;

```

QY      1 MGFEVLLSLATLFGSTSGTALGP...DEVEGLSFARSGGNMAECFA 60
Db      1 MGFEVLLSLATLFGSTSGTALGP...DEVEGLSFARSGGNMAECFA 60
QY      61 SAISPDVDDCRVTFVQVLSRHGARYPTSSAKVSALEALQKNAFAKGYAFKTYN 120
Db      61 SAISPDVDDCRVTFVQVLSRHGARYPTSSAKVSALEALQKNAFAKGYAFKTYN 120
QY      121 YTLGADDLTPFGGNQVNSGIFKFRYKALARKIYVFIASGSDRYASAEKFIQFQSA 180
Db      121 YTLGADDLTPFGGNQVNSGIFKFRYKALARKIYVFIASGSDRYASAEKFIQFQSA 180
QY      181 KLADPGSPHQASPVYINVIIPGSGYNNLTLDGCTAFEDSELGDVQVNAFALFAPAIR 240
Db      181 KLADPGSPHQASPVYINVIIPGSGYNNLTLDGCTAFEDSELGDVQVNAFALFAPAIR 240
QY      241 ARLEADLPQVTLTDEDDVYIYLMDCPFDVARTSDATELSPFCALFTHDEWIQDYLSIG 300
Db      241 ARLEADLPQVTLTDEDDVYIYLMDCPFDVARTSDATELSPFCALFTHDEWIQDYLSIG 300

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Db      241 ARLEAHLPVNLTDDEVYVNLMDMCPDVTARTSDATQLSPECDLFTHDEWIOYDYLQSLG 300
QY      301 KYYGAGNPLGPAOGVGFANELLARLTHSPVODHTSTNHTLDSNPATFPLNATLYADFS 360
Db      301 KYYGAGNPLGPAOGVGFANELLARLTHSPVODHTSTNHTLDSNPATFPLNATLYADFS 360
QY      361 HDNTMISIFPALTNGTSTSTVESIEETDGYASAMTVPFARAVEMMOCEAKEP 420
Db      361 HDNTMISIFPALTNGTSTSTVESIEETDGYASAMTVPFARAVEMMOCEAKEP 420
QY      421 LVRVLVNDRVVPLHGCADVGLGRCKRDEFEGLSFARSGNMACEFA 467
Db      421 LVRVLVNDRVVPLHGCADVGLGRCKRDEFEGLSFARSGNMACEFA 467

RESULT 3
US-09-343-126C-129
; Sequence 129, Application US/09343126C
; GENERAL INFORMATION:
; APPLICANT: Brugger, Roland
; APPLICANT: Lehmann, Martin
; APPLICANT: Wyss, Markus
; TITLE OF INVENTION: Phytase Formulations
; FILE REFERENCE: C38435/109741
; CURRENT APPLICATION NUMBER: US/09/343,126C
; CURRENT FILING DATE: 1999-06-29
; NUMBER OF SEQ ID NOS: 139
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 129
; LENGTH: 467
; TYPE: PRT
; ORGANISM: Consensus sequence
US-09-343-126C-129

```

```

Query Match      95.1%; Score 2342; DB 1; Length 467;
Best Local Similarity 94.4%; Pred. No. 0;
Matches 441; Conservative 10; Mismatches 16; Indels 0; Gaps 0;

QY      1 MGVEFVLISITLFGSTGALGPRGNSHSCDVTGQYCFPEISHLKGTYSPEFLADE 60
Db      1 MGVEFVLISITLFGSTGALGPRGNSHSCDVTGQYCFPEISHLKGTYSPEFLADE 60
QY      61 SAISDVVDDCRVTFVQVLSRHGARYPTSSASKAYSALIAIQNATAFKGAYFLKTYN 120
Db      61 SAISDVVDDCRVTFVQVLSRHGARYPTSSASKAYSALIAIQNATAFKGAYFLKTYN 120
QY      121 YTLGADDLTPGGENOMVNSGIKFRYRKALARKITVPIRASGSDRVYASAKETIEGQSA 180
Db      121 YTLGADDLTPGGENOMVNSGIKFRYRKALARKITVPIRASGSDRVYASAKETIEGQSA 180
QY      181 KLADPGSOPHOASPIYNTIIEPGSGYNNLTDHGTCTAFEESELGDDVEANFTALFAFAR 240
Db      181 KLADPGSOPHOASPIYNTIIEPGSGYNNLTDHGTCTAFEESELGDDVEANFTALFAFAR 240
QY      241 ARLEADLPVNLTDDEVYVNLMDMCPDVTARTSDATELSPECLFTHDEWIOYDYLQSLG 300
Db      241 ARLEADLPVNLTDDEVYVNLMDMCPDVTARTSDATELSPECLFTHDEWIOYDYLQSLG 300
QY      301 KYYGAGNPLGPAOGVGFANELLARLTHSPVODHTSTNHTLDSNPATFPLNATLYADFS 360
Db      301 KYYGAGNPLGPAOGVGFANELLARLTHSPVODHTSTNHTLDSNPATFPLNATLYADFS 360
QY      361 HDNTMISIFPALTNGTSTSTVESIEETDGYASAMTVPFARAVEMMOCEAKEP 420
Db      361 HDNTMISIFPALTNGTSTSTVESIEETDGYASAMTVPFARAVEMMOCEAKEP 420
QY      421 LVRVLVNDRVVPLHGCADVGLGRCKRDEFEGLSFARSGNMACEFA 467
Db      421 LVRVLVNDRVVPLHGCADVGLGRCKRDEFEGLSFARSGNMACEFA 467

```

RESULT 4
US-09-343-126C-130

```

; Sequence 130, Application US/09343126C
; GENERAL INFORMATION:
; APPLICANT: Brugger, Roland
; APPLICANT: Lehmann, Martin
; APPLICANT: Wyss, Markus
; TITLE OF INVENTION: Phytase Formulations
; FILE REFERENCE: C38435/109741
; CURRENT APPLICATION NUMBER: US/09/343,126C
; CURRENT FILING DATE: 1999-06-29
; NUMBER OF SEQ ID NOS: 139
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 130
; LENGTH: 437
; TYPE: PRT
; ORGANISM: Consensus sequence
US-09-343-126C-130

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```

Query Match      83.0%; Score 2044; DB 1; Length 437;
Best Local Similarity 90.4%; Pred. No. 0;
Matches 405; Conservative 7; Mismatches 18; Indels 18; Gaps 10;

QY      27 NSHSCDVTGQYCFPEISHLKGTYSPEFLADESAISPDVDDCRVTFVQVLSRHGARY 86
Db      1 NSHSCDVTGQYCFPEISHLKGTYSPEFLADESAISPDVDDCRVTFVQVLSRHGARY 86
QY      87 PTSSASKAYSALIEAIOKNATAFKGAYFLKTYNTLGAADLTTPGENOMVNSGIKFRYR 146
Db      59 PTSSASKAYSALIERIQKNAT--FKGAYFLKTYNTLGAADLTTPGENOMVNSGIKFRYR 117
QY      147 YKALARKIYPIFIASGSDRVYASAEKEIEGQSAKLADPA---HQAQVINVIIPEGSGY 206
Db      118 YKALARKIYPIFIASGSDRVYASAEKEIEGQSAKLADPA---HQAQVINVIIPEGSGY 174
QY      207 NNTLDHGTCTAFPDSELDGDDVEANFTALFAFARLEADLPVNLTDDEVYVNLMDMCP 266
Db      175 NNTLDHGTCTAFPDSELDGDDVEANFTALFAFARLEADLPVNLTDDEVYVNLMDMCP 233
QY      327 LTHSPVODHTSTNHTLDSNPATFPLNATLYADFSHNTMISIFPALTNGTSTSTSV 386
Db      291 LTHSPVODHTSTNHTLDSNPATFPLNATLYADFSHNTMISIFPALTNGTSTSTSV 350
QY      387 ESIEETDGYASAMTVPFARAVEMMOCEA-----EKEPLRYVYNDRVVPLHGCADV 439
Db      351 ESIEETDGYASAMTVPFARAVEMMOCEAGGCGGEGEKEPELVRLVNDRVVPLHGCADV 409
QY      440 KLGRCKRDPFVEGLSFARSGNMACEFA 467
Db      410 KLGRCKRDPFVEGLSFARSGNMACEFA 437

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Search completed: March 20, 2003, 08:23:06
Job time : 0.001 secs

GenCore version 5.1.4-p5_4578
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OM protein - protein search, using sw model

Run on: March 20, 2003, 08:24:15 ; Search time 0.001 Seconds

(without alignments)
858.346 Million cell updates/sec

Title: us-09-488-265-31

Perfect score: 2468

Sequence: 1 MGVEVVLSTATLFGSGTSGT.....DFVEGLSFARSGNNEECFA 467

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 4 segs, 1838 residues

Total number of hits satisfying chosen parameters: 4

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: ramirez126.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2468	100.0	467	1	US-09-343-126C-134
2	2448	99.2	467	1	US-09-343-126C-129
3	2362	95.7	467	1	US-09-343-126C-132
4	2093	84.8	437	1	US-09-343-126C-130

ALIGNMENTS

RESULT 1

US-09-343-126C-134

; Sequence 134, Application US/09343126C

; GENERAL INFORMATION:

; APPLICANT: Bruggier, Roland

; APPLICANT: Lehmann, Martin

; APPLICANT: Wyses, Markus

; TITLE OF INVENTION: Phytase Formulations

; FILE REFERENCE: C38435/109741

; CURRENT APPLICATION NUMBER: US/09/343,126C

; CURRENT FILING DATE: 1999-06-29

; NUMBER OF SEQ ID NOS: 139

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 134

; LENGTH: 467

; TYPE: PRT

; ORGANISM: Consensus sequence

US-09-343-126C-134

Query Match 100.0%; Score 2468; DB 1; Length 467;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 467; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MGVEVVLSTATLFGSGTSGTALGPRGNSHSCDVTVDGTYQCFPEISHLMGTYSPPFSLADE 60

Db 1 MGVEVVLSTATLFGSGTSGTALGPRGNSHSCDVTVDGTYQCFPEISHLMGTYSPPFSLADE 60

OY 61 SAISPDVPGKGRVTFVQVLSRHGARYPTSSAKAYSALEIAIOKNATFAFGKATFLKTYN 120

Db 61 SAISPDVPGKGRVTFVQVLSRHGARYPTSSAKAYSALEIAIOKNATFAFGKATFLKTYN 120

OY 121 YTLGADDLTPFGEOQWNSGIKFYRRKALARKIVPEIRASGSDRYIASAEKPIEGFQSA 180

Db 121 YTLGADDLTPFGEOQWNSGIKFYRRKALARKIVPEIRASGSDRYIASAEKPIEGFQSA 180

OY 181 KLADPGANPHQASPVINVIIPGAGYNNTLDHGLCTAFESSELDGDDVEANFAVEAPR 240

Db 181 KLADPGANPHQASPVINVIIPGAGYNNTLDHGLCTAFESSELDGDDVEANFAVEAPR 240

OY 241 ARLEAHLPGVNLDEDEVNIMDMCPDVTVAARTSDATQLSPCDLPFTHDEMIQDYLSIG 300

Db 241 ARLEAHLPGVNLDEDEVNIMDMCPDVTVAARTSDATQLSPCDLPFTHDEMIQDYLSIG 300

OY 301 KYGYGAGNPLGPAQGVGFVNEIARLTHSPVODHTSTNHTLDSNATPPLNATLYADFS 360

Db 301 KYGYGAGNPLGPAQGVGFVNEIARLTHSPVODHTSTNHTLDSNATPPLNATLYADFS 360

OY 361 HDNTWYSIFPALGYNKTRPLSTTSVESIEETDGYASATVPFARAYEMQCEAEKRP 420

Db 361 HDNTWYSIFPALGYNKTRPLSTTSVESIEETDGYASATVPFARAYEMQCEAEKRP 420

OY 421 LVRLVYNDRVVPLHGGGVKLGRCRDPDFEGLSFARSGNNEECFA 467

Db 421 LVRLVYNDRVVPLHGGGVKLGRCRDPDFEGLSFARSGNNEECFA 467

RESULT 2

US-09-343-126C-129

; Sequence 129, Application US/09343126C

; GENERAL INFORMATION:

; APPLICANT: Bruggier, Roland

; APPLICANT: Lehmann, Martin

; APPLICANT: Wyses, Markus

; TITLE OF INVENTION: Phytase Formulations

; FILE REFERENCE: C38435/109741

; CURRENT APPLICATION NUMBER: US/09/343,126C

; CURRENT FILING DATE: 1999-06-29

; NUMBER OF SEQ ID NOS: 139

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 129

; LENGTH: 467

; TYPE: PRT

; ORGANISM: Consensus sequence

US-09-343-126C-129

Query Match 99.2%; Score 2448; DB 1; Length 467;

Best Local Similarity 98.9%; Pred. No. 0;

Matches 462; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 1 MGVEVVLSTATLFGSGTSGTALGPRGNSHSCDVTVDGTYQCFPEISHLMGTYSPPFSLADE 60

Db 1 MGVEVVLSTATLFGSGTSGTALGPRGNSHSCDVTVDGTYQCFPEISHLMGTYSPPFSLADE 60

OY 61 SAISPDVPGKGRVTFVQVLSRHGARYPTSSAKAYSALEIAIOKNATFAFGKATFLKTYN 120

Db 61 SAISPDVPGKGRVTFVQVLSRHGARYPTSSAKAYSALEIAIOKNATFAFGKATFLKTYN 120

OY 121 YTLGADDLTPFGEOQWNSGIKFYRRKALARKIVPEIRASGSDRYIASAEKPIEGFQSA 180

Db 121 YTLGADDLTPFGEOQWNSGIKFYRRKALARKIVPEIRASGSDRYIASAEKPIEGFQSA 180

OY 181 KLADPGANPHQASPVINVIIPGAGYNNTLDHGLCTAFESSELDGDDVEANFAVEAPR 240

Db 181 KLADPGANPHQASPVINVIIPGAGYNNTLDHGLCTAFESSELDGDDVEANFAVEAPR 240

OY 241 ARLEAHLPGVNLDEDEVNIMDMCPDVTVAARTSDATQLSPCDLPFTHDEMIQDYLSIG 300

Db 241 ARLEAHLPGVNLDEDEVNIMDMCPDVTVAARTSDATQLSPCDLPFTHDEMIQDYLSIG 300

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Db 241 ARLEAHLPGVNLDEDEVYNNLMDMCPDVTVA RTSDA TQ LSPFCDLFTHDEWIQYDIQSLG 300
; Sequence 132, Application US/09343126C
; GENERAL INFORMATION:
; APPLICANT: Brugger, Roland
; APPLICANT: Lehmann, Martin
; APPLICANT: Wysz, Markus
; TITLE OF INVENTION: Phytase Formulations
; FILE REFERENCE: C38435/109741
; CURRENT APPLICATION NUMBER: US/09/343.126C
; CURRENT FILING DATE: 1999-06-29
; NUMBER OF SEQ ID NOS: 139
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 132
; LENGTH: 467
; TYPE: PRT
; ORGANISM: Consensus sequence
US-09-343-126C-132

Query Match          95.7%; Score 2362; DB 1; Length 467;
Best Local Similarity 95.5%; Pred. No. 0;
Matches 446; Conservative 8; Mismatches 13; Indels 0; Gaps 0;

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QY 1 MGVEVLLSTATLFGSTSGTALGPRGNHSCDTVDGTCOCPELSHLMGTSPFSLADE 60
Db 1 MGVEVLLSTATLFGSTSGTALGPRGNHSCDTVDGTCOCPELSHLMGTSPFSLADE 60
QY 61 SAISPDVPCRTYFVOVLSRHGARYPTSSASKAYSALEIOLKNTAFKGYAFLKTYN 120
Db 61 SAISPDVPCRTYFVOVLSRHGARYPTSSASKAYSALEIOLKNTAFKGYAFLKTYN 120
QY 121 YTLGADDLTPFGEQOMVNSGIRKRYRKALARKIVPPIRASGSDRYIASAEKIEGQSA 180
Db 121 YTLGADDLTPFGEQOMVNSGIRKRYRKALARKIVPPIRASGSDRYIASAEKIEGQSA 180
QY 181 KLADEGANPHQASPIVITVITPEAGYNNLTLDHGLCTAFEESELDGDDVEANFTAVFAPPIR 240
Db 181 KLADEGANPHQASPIVITVITPEAGYNNLTLDHGLCTAFEESELDGDDVEANFTAVFAPPIR 240
QY 241 ARLEAHLPGVNLDEDEVYNNLMDMCPDVTVA RTSDA TQ LSPFCDLFTHDEWIQYDIQSLG 300
Db 241 ARLEAHLPGVNLDEDEVYNNLMDMCPDVTVA RTSDA TQ LSPFCDLFTHDEWIQYDIQSLG 300
QY 301 KYTGAGNPLGPAQGVGFVVELLARTLHSPVODHTSTNHTLDSNPATFPPLNATLYADFS 360
Db 301 KYTGAGNPLGPAQGVGFVVELLARTLHSPVODHTSTNHTLDSNPATFPPLNATLYADFS 360
QY 361 HDNMTVSIFFFALGLYNGKPLSTSVESIEETDGYASWTVPFARAYVEMMOCEAKEP 420
Db 361 HDNMTVSIFFFALGLYNGKPLSTSVESIEETDGYASWTVPFARAYVEMMOCEAKEP 420
QY 421 LVRVLVNDRVVPLHGGVVDKLGRCRDKDFVEGLSFARSGGWMACEFA 467
Db 421 LVRVLVNDRVVPLHGGVVDKLGRCRDKDFVEGLSFARSGGWMACEFA 467

```

RESULT 4
US-09-343-126C-130

```

; Sequence 130, Application US/09343126C
; GENERAL INFORMATION:
; APPLICANT: Brugger, Roland
; APPLICANT: Lehmann, Martin
; APPLICANT: Wysz, Markus
; TITLE OF INVENTION: Phytase Formulations
; FILE REFERENCE: C38435/109741
; CURRENT APPLICATION NUMBER: US/09/343.126C
; CURRENT FILING DATE: 1999-06-29
; NUMBER OF SEQ ID NOS: 139
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 130
; LENGTH: 437
; TYPE: PRT
; ORGANISM: Consensus sequence
US-09-343-126C-130

Query Match          84.8%; Score 2093; DB 1; Length 437;
Best Local Similarity 92.4%; Pred. No. 0;
Matches 414; Conservative 4; Mismatches 12; Indels 18; Gaps 10;

```

```

QY 27 NSHSCDTVDGTCOCPELSHLMGTSPFSLADESALSPDVPCGCRVTEVYLSRHGARY 86
Db 1 NSHSCDTVD-GYOC-PELSHLMGTSPFSLADESALSPDVPCGCRVTEVYLSRHGARY 86
QY 87 PTSSASKAYSALEIOLKNTAFKGYAFLKTYNYTLGADDLTPFGEQOMVNSGIRKRYR 146
Db 59 PTSSASKAYSALEIOLKNTAFKGYAFLKTYNYTLGADDLTPFGEQOMVNSGIRKRYR 117
QY 147 YKALARKIVPPIRASGSDRYIASAEKIEGQSAKLADPGANPHQASPIVITVITPEAGY 206
Db 118 YKALARKIVPPIRASGSDRYIASAEKIEGQSAKLADPA---HQASPIVITVITPEAGY 174
QY 207 NNTLDHGLCTAFEESELDGDDVEANFTAVFAPPIRARTLHSPVODHTSTNHTLDSNPATFPPLNATLYADFS 266
Db 175 NNTLDHGLCTAFEESELDGDDVEANFTAVFAPPIRARTLHSPVODHTSTNHTLDSNPATFPPLNATLYADFS 233
QY 267 DTVARTSDATQ LSPFCDLFTHDEWIQYDIQSLGKYGYGAGNPLGPAQGVGFVVELLART 326
Db 234 DTVARTSDATQ LSPFCDLFTHDEWIQYDIQSLGKYGYGAGNPLGPAQGVGFVVELLART 290
QY 327 LTHSPVODHTSTNHTLDSNPATFPPLNATLYADFSHNTMWSIFALGLYNGKPLSTTSV 386
Db 291 LTHSPVODHTSTNHTLDSNPATFPPLNATLYADFSHNTMWSIFALGLYNGKPLSTTSV 350
QY 387 ESIEETDGYASWTVPFARAYVEMMOCEA-----EKEPLVAVLNDRVVPLHGGCYD 439
Db 351 ES1-ETDGYASWTVPFARAYVEMMOCEAGGGEKEPLVAVLNDRVVPLHGGCYD 409
QY 440 KIGRCRDKDFVEGLSFARSGGWMACEFA 467
Db 410 KIGRCRDKDFVEGLSFARSGGWMACEFA 437

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Search completed: March 20, 2003, 08:24:16
Job time : 1 secs